



IFWO

## RAW SEQUENCE LISTING

DATE: 08/06/2004

PATENT APPLICATION: US/10/808,187A

TIME: 11:28:54

Input Set : D:\V9661078.app

Output Set: N:\CRF4\08062004\J808187A.raw

3 <110> APPLICANT: PEIRIS, JOSEPH S. M.  
 4 YUEN, KWOK YUNG  
 5 POON, LIT MAN  
 6 GUAN, YI  
 7 CHAN, KWOK HUNG  
 8 NICHOLLS, JOHN  
 10 <120> TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE  
 11 RESPIRATORY SYNDROME (SARS)  
 13 <130> FILE REFERENCE: V9661.0078  
 15 <140> CURRENT APPLICATION NUMBER: 10/808,187A  
 16 <141> CURRENT FILING DATE: 2004-03-24  
 18 <150> PRIOR APPLICATION NUMBER: 60/457,031  
 19 <151> PRIOR FILING DATE: 2003-03-24  
 21 <150> PRIOR APPLICATION NUMBER: 60/457,730  
 22 <151> PRIOR FILING DATE: 2003-03-26  
 24 <150> PRIOR APPLICATION NUMBER: 60/459,931  
 25 <151> PRIOR FILING DATE: 2003-04-02  
 27 <150> PRIOR APPLICATION NUMBER: 60/460,357  
 28 <151> PRIOR FILING DATE: 2003-04-03  
 30 <150> PRIOR APPLICATION NUMBER: 60/461,265  
 31 <151> PRIOR FILING DATE: 2003-04-08  
 33 <150> PRIOR APPLICATION NUMBER: 60/462,805  
 34 <151> PRIOR FILING DATE: 2003-04-14  
 36 <150> PRIOR APPLICATION NUMBER: 60/468,139  
 37 <151> PRIOR FILING DATE: 2003-05-05  
 39 <150> PRIOR APPLICATION NUMBER: 60/464,886  
 40 <151> PRIOR FILING DATE: 2003-04-23  
 42 <150> PRIOR APPLICATION NUMBER: 60/471,200  
 43 <151> PRIOR FILING DATE: 2003-05-16  
 45 <160> NUMBER OF SEQ ID NOS: 2476  
 47 <170> SOFTWARE: PatentIn ver. 3.2  
 49 <210> SEQ ID NO: 1  
 50 <211> LENGTH: 646  
 51 <212> TYPE: DNA  
 52 <213> ORGANISM: Human severe acute respiratory syndrome virus  
 54 <220> FEATURE:  
 55 <221> NAME/KEY: CDS  
 56 <222> LOCATION: (2)...(646)  
 58 <400> SEQUENCE: 1  
 59 a cag gac gct gta gct tca aaa atc tta gga ttg cct acg cag act gtt 49  
 60 Gln Asp Ala Val Ala Ser Lys Ile Leu Gly Leu Pro Thr Gln Thr Val  
 61 1 5 10 15  
 63 gat tca tca cag ggt tct gaa tat gac tat gtc ata ttc aca caa act 97



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64 Asp Ser Ser Gln Gly Ser Glu Tyr Asp Tyr Val Ile Phe Thr Gln Thr
65          20          25          30
67 act gaa aca gca cac tct tgt aat gtc aac cgc ttc aat gtg gct atc 145
68 Thr Glu Thr Ala His Ser Cys Asn Val Asn Arg Phe Asn Val Ala Ile
69          35          40          45
71 aca agg gca aaa att ggc att ttg tgc ata atg tct gat aga gat ctt 193
72 Thr Arg Ala Lys Ile Gly Ile Leu Cys Ile Met Ser Asp Arg Asp Leu
73          50          55          60
75 tat gac aaa ctg caa ttt aca agt cta gaa ata cca cgt cgc aat gtg 241
76 Tyr Asp Lys Leu Gln Phe Thr Ser Leu Glu Ile Pro Arg Arg Asn Val
77 65          70          75          80
79 gct aca tta caa gca gaa aat gta act gga ctt ttt aag gac tgt agt 289
80 Ala Thr Leu Gln Ala Glu Asn Val Thr Gly Leu Phe Lys Asp Cys Ser
81          85          90          95
83 aag atc att act ggt ctt cat cct aca cag gca cct aca cac ctc agc 337
84 Lys Ile Ile Thr Gly Leu His Pro Thr Gln Ala Pro Thr His Leu Ser
85          100          105          110
87 gtt gat ata aaa ttc aag act gaa gga tta tgt gtt gac ata cca ggc 385
88 Val Asp Ile Lys Phe Lys Thr Glu Gly Leu Cys Val Asp Ile Pro Gly
89          115          120          125
91 ata cca aag gac atg acc tac cgt aga ctc atc tct atg atg ggt ttc 433
92 Ile Pro Lys Asp Met Thr Tyr Arg Arg Leu Ile Ser Met Met Gly Phe
93          130          135          140
95 aaa atg aat tac caa gtc aat ggt tac cct aat atg ttt atc acc cgc 481
96 Lys Met Asn Tyr Gln Val Asn Gly Tyr Pro Asn Met Phe Ile Thr Arg
97 145          150          155          160
99 gaa gaa gct att cgt cac gtt cgt gcg tgg att ggc ttt gat gta gag 529
100 Glu Glu Ala Ile Arg His Val Arg Ala Trp Ile Gly Phe Asp Val Glu
101          165          170          175
103 ggc tgt cat gca act aga gat gct gtg ggt act aac cta cct ctc cag 577
104 Gly Cys His Ala Thr Arg Asp Ala Val Gly Thr Asn Leu Pro Leu Gln
105          180          185          190
107 cta gga ttt tct aca ggt gtt aac tta gta gct gta ccg act ggt tat 625
108 Leu Gly Phe Ser Thr Gly Val Asn Leu Val Ala Val Pro Thr Gly Tyr
109          195          200          205
111 gtt gac act gaa aat aac cta 646
112 Val Asp Thr Glu Asn Asn Leu
113          210          215
116 <210> SEQ ID NO: 2
117 <211> LENGTH: 215
118 <212> TYPE: PRT
119 <213> ORGANISM: Human severe acute respiratory syndrome virus
121 <400> SEQUENCE: 2
122 Gln Asp Ala Val Ala Ser Lys Ile Leu Gly Leu Pro Thr Gln Thr Val
123 1          5          10          15
125 Asp Ser Ser Gln Gly Ser Glu Tyr Asp Tyr Val Ile Phe Thr Gln Thr
126          20          25          30
128 Thr Glu Thr Ala His Ser Cys Asn Val Asn Arg Phe Asn Val Ala Ile
129          35          40          45

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131 Thr Arg Ala Lys Ile Gly Ile Leu Cys Ile Met Ser Asp Arg Asp Leu
132      50                      55                      60
134 Tyr Asp Lys Leu Gln Phe Thr Ser Leu Glu Ile Pro Arg Arg Asn Val
135 65                      70                      75                      80
137 Ala Thr Leu Gln Ala Glu Asn Val Thr Gly Leu Phe Lys Asp Cys Ser
138                      85                      90                      95
140 Lys Ile Ile Thr Gly Leu His Pro Thr Gln Ala Pro Thr His Leu Ser
141                      100                     105                     110
143 Val Asp Ile Lys Phe Lys Thr Glu Gly Leu Cys Val Asp Ile Pro Gly
144                      115                     120                     125
146 Ile Pro Lys Asp Met Thr Tyr Arg Arg Leu Ile Ser Met Met Gly Phe
147      130                      135                      140
149 Lys Met Asn Tyr Gln Val Asn Gly Tyr Pro Asn Met Phe Ile Thr Arg
150 145                      150                      155                      160
152 Glu Glu Ala Ile Arg His Val Arg Ala Trp Ile Gly Phe Asp Val Glu
153                      165                      170                      175
155 Gly Cys His Ala Thr Arg Asp Ala Val Gly Thr Asn Leu Pro Leu Gln
156                      180                      185                      190
158 Leu Gly Phe Ser Thr Gly Val Asn Leu Val Ala Val Pro Thr Gly Tyr
159      195                      200                      205
161 Val Asp Thr Glu Asn Asn Leu
162      210                      215
165 <210> SEQ ID NO: 3
166 <211> LENGTH: 17
167 <212> TYPE: DNA
168 <213> ORGANISM: Artificial Sequence
170 <220> FEATURE:
171 <223> OTHER INFORMATION: primer sequence for RT-PCT based on partial
172     nucleotide sequence of the genome of hSARS
174 <400> SEQUENCE: 3
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177 <210> SEQ ID NO: 4
178 <211> LENGTH: 16
179 <212> TYPE: DNA
180 <213> ORGANISM: Artificial Sequence
182 <220> FEATURE:
183 <223> OTHER INFORMATION: primer sequence for RT-PCT based on partial
184     nucleotide sequence of the genome of hSARS
186 <400> SEQUENCE: 4
187 cacgaacgtg acgaat                                     16
189 <210> SEQ ID NO: 5
190 <211> LENGTH: 27
191 <212> TYPE: DNA
192 <213> ORGANISM: Artificial Sequence
194 <220> FEATURE:
195 <223> OTHER INFORMATION: degenerated primer in Superscript II Kit by
196     Invitrogen
198 <220> FEATURE:
199 <221> NAME/KEY: misc_feature

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200 <222> LOCATION: (21)..(27)
201 <223> OTHER INFORMATION: a, t, c or g
203 <400> SEQUENCE: 5
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207 <211> LENGTH: 20
208 <212> TYPE: DNA
209 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <223> OTHER INFORMATION: primer provided in AmpliTaq Gold Kit by Applied
213 Biosyndromes
215 <400> SEQUENCE: 6
216 gccggagctc tgcagaattc 20
218 <210> SEQ ID NO: 7
219 <211> LENGTH: 17
220 <212> TYPE: DNA
221 <213> ORGANISM: Artificial Sequence
223 <220> FEATURE:
224 <223> OTHER INFORMATION: First round of primer for amplifying human
225 metapneumovirus (HMPV)
227 <400> SEQUENCE: 7
228 aargtsaatg catcagc 17
230 <210> SEQ ID NO: 8
231 <211> LENGTH: 20
232 <212> TYPE: DNA
233 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
236 <223> OTHER INFORMATION: first round primer for amplifying human
237 metapneumovirus (HMPV)
239 <400> SEQUENCE: 8
240 cakattytgc ttatgctttc 20
242 <210> SEQ ID NO: 9
243 <211> LENGTH: 20
244 <212> TYPE: DNA
245 <213> ORGANISM: Artificial Sequence
247 <220> FEATURE:
248 <223> OTHER INFORMATION: nested primer for amplifying human metapneumovirus
249 (HMPV)
251 <400> SEQUENCE: 9
252 acacctgtta caataccagc 20
254 <210> SEQ ID NO: 10
255 <211> LENGTH: 19
256 <212> TYPE: DNA
257 <213> ORGANISM: Artificial Sequence
259 <220> FEATURE:
260 <223> OTHER INFORMATION: nested primer for amplifying human metapneumovirus
261 (HMPV)
263 <400> SEQUENCE: 10
264 gacttgagtc ccagctcca 19

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Input Set : D:\V9661078.app

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266 <210> SEQ ID NO: 11
267 <211> LENGTH: 1213
268 <212> TYPE: DNA
269 <213> ORGANISM: Human severe acute respiratory syndrome virus
271 <220> FEATURE:
272 <221> NAME/KEY: CDS
273 <222> LOCATION: (2)...(1213)
275 <400> SEQUENCE: 11
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277   Lys Cys Ser Arg Ile Ile Pro Ala Arg Ala Arg Val Glu Cys Phe Asp
278   1         5         10        15
280 aaa ttc aaa gtg aat tca aca cta gaa cag tat gtt ttc tgc act gta 97
281 Lys Phe Lys Val Asn Ser Thr Leu Glu Tyr Val Phe Cys Thr Val
282   20        25        30
284 aat gca ttg cca gaa aca act gct gac att gta gtc ttt gat gaa atc 145
285 Asn Ala Leu Pro Glu Thr Thr Ala Asp Ile Val Val Phe Asp Glu Ile
286   35        40        45
288 tct atg gct act aat tat gac ttg agt gtt gtc aat gct aga ctt cgt 193
289 Ser Met Ala Thr Asn Tyr Asp Leu Ser Val Val Asn Ala Arg Leu Arg
290   50        55        60
292 gca aaa cac tac gtc tat att ggc gat cct gct caa tta cca gcc ccc 241
293 Ala Lys His Tyr Val Tyr Ile Gly Asp Pro Ala Gln Leu Pro Ala Pro
294 65         70         75         80
296 cgc aca ttg ctg act aaa ggc aca cta gaa cca gaa tat ttt aat tca 289
297 Arg Thr Leu Leu Thr Lys Gly Thr Leu Glu Pro Glu Tyr Phe Asn Ser
298   85        90        95
300 gtg tgc aga ctt atg aaa aca ata ggt cca gac atg ttc ctt gga act 337
301 Val Cys Arg Leu Met Lys Thr Ile Gly Pro Asp Met Phe Leu Gly Thr
302 100       105       110
304 tgt cgc cgt tgt cct gct gaa att gtt gac act gtg agt gct tta gtt 385
305 Cys Arg Arg Cys Pro Ala Glu Ile Val Asp Thr Val Ser Ala Leu Val
306 115       120       125
308 tat gac aat aag cta aaa gca cac aag gag aag tca gct caa tgc ttc 433
309 Tyr Asp Asn Lys Leu Lys Ala His Lys Glu Lys Ser Ala Gln Cys Phe
310 130       135       140
312 aaa atg ttc tac aaa ggt gtt att aca cat gat gtt tca tct gca atc 481
313 Lys Met Phe Tyr Lys Gly Val Ile Thr His Asp Val Ser Ser Ala Ile
314 145       150       155       160
316 aac aga cct caa ata ggc gtt gta aga gaa ttt ctt aca cgc aat cct 529
317 Asn Arg Pro Gln Ile Gly Val Val Arg Glu Phe Leu Thr Arg Asn Pro
318 165       170       175
320 gct tgg aga aaa gct gtt ttt atc tca cct tat aat tca cag aac gct 577
321 Ala Trp Arg Lys Ala Val Phe Ile Ser Pro Tyr Asn Ser Gln Asn Ala
322 180       185       190
324 gta gct tca aaa atc tta gga ttg cct acg cag act gtt gat tca tca 625
325 Val Ala Ser Lys Ile Leu Gly Leu Pro Thr Gln Thr Val Asp Ser Ser
326 195       200       205
328 cag ggt tct gaa tat gac tat gtc ata ttc aca caa act act gaa aca 673
329 Gln Gly Ser Glu Tyr Asp Tyr Val Ile Phe Thr Gln Thr Thr Glu Thr

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RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 08/06/2004  
PATENT APPLICATION:    US/10/808,187A      TIME: 11:28:55

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 21,22,23,24,25,26,27

VERIFICATION SUMMARY

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Input Set : D:\V9661078.app

Output Set: N:\CRF4\08062004\J808187A.raw

L:204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0